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RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/09/874,389

TIME: 14:52:51

Input Set : N:\Crf3\RULE60\09874389.txt

Output Set: N:\CRF3\01152002\I874389.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Bujard, Hermann

6 Gossen, Manfred

8 (ii) TITLE OF INVENTION: Animal Transgenic for a Tetracycline- Inducible
9 Transcription

11 (iii) NUMBER OF SEQUENCES: 28

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: LAHIVE & COCKFIELD

15 (B) STREET: 60 State Street, Suite 510

16 (C) CITY: Boston

17 (D) STATE: Massachusetts

18 (E) COUNTRY: USA

19 (F) ZIP: 02109-1875

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: ASCII Text

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/874,389

C--> 29 (B) FILING DATE: 26-Dec-2001

60 (C) CLASSIFICATION:

57 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 09/161,902

34 (B) FILING DATE:

38 (A) APPLICATION NUMBER: US 08/275,876

39 (B) FILING DATE: 15-JULY-1994

43 (A) APPLICATION NUMBER: US 08/270,637

44 (B) FILING DATE: 01-JULY-94

48 (A) APPLICATION NUMBER: US 08/260,452

49 (B) FILING DATE: 14-JUNE-1994

53 (A) APPLICATION NUMBER: US 08/076,327

54 (B) FILING DATE: 14-JUNE-1993

58 (A) APPLICATION NUMBER: US 08/076,726

59 (B) FILING DATE: 14-JUNE-1993

62 (viii) ATTORNEY/AGENT INFORMATION:

63 (A) NAME: DeConti, Giulio A. Jr.

64 (B) REGISTRATION NUMBER: 31,503

65 (C) REFERENCE/DOCKET NUMBER: BBI-009CP3

67 (ix) TELECOMMUNICATION INFORMATION:

68 (A) TELEPHONE: (617)227-7400

69 (B) TELEFAX: (617)227-5941

ENTERED

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72 (2) INFORMATION FOR SEQ ID NO: 1:

74 (i) SEQUENCE CHARACTERISTICS:

75 (A) LENGTH: 1008 base pairs

76 (B) TYPE: nucleic acid

77 (C) STRANDEDNESS: double

78 (D) TOPOLOGY: linear

W--> 80 (ii) MOLECULE TYPE: DNA

82 (ix) FEATURE:

83 (A) NAME/KEY: exon

84 (B) LOCATION: 1..1008

86 (ix) FEATURE:

87 (A) NAME/KEY: mRNA

88 (B) LOCATION: 1..1008

90 (ix) FEATURE:

91 (A) NAME/KEY: misc. binding

92 (B) LOCATION: 1..207

94 (ix) FEATURE:

95 (A) NAME/KEY: misc. binding

96 (B) LOCATION: 208..335

98 (ix) FEATURE:

99 (A) NAME/KEY: CDS

100 (B) LOCATION: 1..1005

102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

103	ATG	TCT	AGA	TTA	GAT	AAA	AGT	AAA	GTG	ATT	AAC	AGC	GCA	TTA	GAG	CTG	48
104	Met	Ser	Arg	Leu	Asp	Lys	Ser	Lys	Val	Ile	Asn	Ser	Ala	Leu	Glu	Leu	
105	1				5				10						15		
107	CTT	AAT	GAG	GTC	GGA	ATC	GAA	GGT	TTA	ACA	ACC	CGT	AAA	CTC	GCC	CAG	96
108	Leu	Asn	Glu	Val	Gly	Ile	Glu	Gly	Leu	Thr	Thr	Arg	Lys	Leu	Ala	Gln	
109				20				25						30			
111	AAG	CTA	GGT	GTA	GAG	CAG	CCT	ACA	CTG	TAT	TGG	CAT	GTA	AAA	AAT	AAG	144
112	Lys	Leu	Gly	Val	Glu	Gln	Pro	Thr	Leu	Tyr	Trp	His	Val	Lys	Asn	Lys	
113			35				40						45				
115	CGG	GCT	TTG	CTC	GAC	GCC	TTA	GCC	ATT	GAG	ATG	TTA	GAT	AGG	CAC	CAT	192
116	Arg	Ala	Leu	Leu	Asp	Ala	Leu	Ala	Ile	Glu	Met	Leu	Asp	Arg	His	His	
117		50				55				60							
119	ACT	CAC	TTT	TGC	CCT	TTA	AAA	GGG	GAA	AGC	TGG	CAA	GAT	TTT	TTA	CGC	240
120	Thr	His	Phe	Cys	Pro	Leu	Lys	Gly	Glu	Ser	Trp	Gln	Asp	Phe	Leu	Arg	
121	65				70				75					80			
123	AAT	AAG	GCT	AAA	AGT	TTT	AGA	TGT	GCT	TTA	CTA	AGT	CAT	CGC	AAT	GGA	288
124	Asn	Lys	Ala	Lys	Ser	Phe	Arg	Cys	Ala	Leu	Leu	Ser	His	Arg	Asn	Gly	
125			85					90					95				
127	GCA	AAA	GTA	CAT	TCA	GAT	ACA	CGG	CCT	ACA	GAA	AAA	CAG	TAT	GAA	ACT	336
128	Ala	Lys	Val	His	Ser	Asp	Thr	Arg	Pro	Thr	Glu	Lys	Gln	Tyr	Glu	Thr	
129			100					105					110				
131	CTC	GAA	AAT	CAA	TTA	GCC	TTT	TTA	TGC	CAA	CAA	GGT	TTT	TCA	CTA	GAG	384
132	Leu	Glu	Asn	Gln	Leu	Ala	Phe	Leu	Cys	Gln	Gln	Gly	Phe	Ser	Leu	Glu	
133			115				120					125					
135	AAT	GCA	TTA	TAT	GCA	CTC	AGC	GCT	GTG	GGG	CAT	TTT	ACT	TTA	GGT	TGC	432
136	Asn	Ala	Leu	Tyr	Ala	Leu	Ser	Ala	Val	Gly	His	Phe	Thr	Leu	Gly	Cys	

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137      130      135      140
139 GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA      480
140 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
141 145      150      155      160
143 CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA      528
144 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
145      165      170      175
147 TTT GAT CAC CAA GGT GCA GAG CCA GCC TTC TTA TTC GGC CTT GAA TTG      576
148 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
149      180      185      190
151 ATC ATA TGC GGA TTA GAA AAA CAA CTT AAA TGT GAA AGT GGG TCC GCG      624
152 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
153      195      200      205
155 TAC AGC CGC GCG CGT ACG AAA AAC AAT TAC GGG TCT ACC ATC GAG GGC      672
156 Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
157      210      215      220
159 CTG CTC GAT CTC CCG GAC GAC GAC GCC CCC GAA GAG GCG GGG CTG GCG      720
160 Leu Leu Asp Leu Pro Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
161 225      230      235      240
163 GCT CCG CGC CTG TCC TTT CTC CCC GCG GGA CAC ACG CGC AGA CTG TCG      768
164 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
165      245      250      255
167 ACG GCC CCC CCG ACC GAT GTC AGC CTG GGG GAC GAG CTC CAC TTA GAC      816
168 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
169      260      265      270
171 GGC GAG GAC GTG GCG ATG GCG CAT GCC GAC GCG CTA GAC GAT TTC GAT      864
172 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
173      275      280      285
175 CTG GAC ATG TTG GGG GAC GGG GAT TCC CCG GGT CCG GGA TTT ACC CCC      912
176 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
177      290      295      300
179 CAC GAC TCC GCC CCC TAC GGC GCT CTG GAT ATG GCC GAC TTC GAG TTT      960
180 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
181 305      310      315      320
183 GAG CAG ATG TTT ACC GAT CCC CTT GGA ATT GAC GAG TAC GGT GGG TAG      1008
184 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
185      325      330      335

```

187 (2) INFORMATION FOR SEQ ID NO: 2:

188 (i) SEQUENCE CHARACTERISTICS:

189 (A) LENGTH: 335 amino acids

190 (B) TYPE: amino acid

191 (D) TOPOLOGY: linear

192 (ii) MOLECULE TYPE: protein

193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

194 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
195 1      5      10      15
197 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
198      20      25      30
200 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys

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```

201          35          40          45
203 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
204          50          55          60
206 Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
207 65          70          75          80
209 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly
210          85          90          95
212 Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
213          100          105          110
215 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
216          115          120          125
218 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
219          130          135          140
221 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
222 145          150          155          160
224 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
225          165          170          175
227 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
228          180          185          190
230 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
231          195          200          205
233 Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
234          210          215          220
236 Leu Leu Asp Leu Pro Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
237 225          230          235          240
239 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
240          245          250          255
242 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
243          260          265          270
245 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
246          275          280          285
248 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
249          290          295          300
251 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
252 305          310          315          320
254 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
255          325          330          335

```

258 (2) INFORMATION FOR SEQ ID NO: 3:

260 (i) SEQUENCE CHARACTERISTICS:

261 (A) LENGTH: 33 base pairs

262 (B) TYPE: nucleic acid

263 (C) STRANDEDNESS: double

264 (D) TOPOLOGY: linear

W--> 266 (ii) MOLECULE TYPE: DNA

268 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

270 GAC GCG CTA GAC GAT TTC GAT CTG GAC ATG TTG 33

271 Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu

272 1 5 10

275 (2) INFORMATION FOR SEQ ID NO: 4:

RAW SEQUENCE LISTING

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```

277      (i) SEQUENCE CHARACTERISTICS:
278          (A) LENGTH: 11 amino acids
279          (B) TYPE: amino acid
280          (D) TOPOLOGY: linear
282      (ii) MOLECULE TYPE: peptide
284      (v) FRAGMENT TYPE: internal
288      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
290      Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
291          1             5             10
293 (2) INFORMATION FOR SEQ ID NO: 5:
295      (i) SEQUENCE CHARACTERISTICS:
296          (A) LENGTH: 7 amino acids
297          (B) TYPE: amino acid
298          (D) TOPOLOGY: linear
300      (ii) MOLECULE TYPE: peptide
302      (v) FRAGMENT TYPE: internal
306      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
308      Met Pro Lys Arg Pro Arg Pro
309          1             5
311 (2) INFORMATION FOR SEQ ID NO: 6:
313      (i) SEQUENCE CHARACTERISTICS:
314          (A) LENGTH: 569 base pairs
315          (B) TYPE: nucleic acid
316          (C) STRANDEDNESS: double
317          (D) TOPOLOGY: linear
W--> 319      (ii) MOLECULE TYPE: DNA
323      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
325      GAATTCGGGG CCGCGGAGGC TGGATCGGTC CCGGTGTCTT CTATGGAGGT CAAAACAGCG      60
327      TGGATGGCGT CTCCAGGCGA TCTGACGGTT CACTAAACGA GCTCTGCTTA TATAGGTCGA      120
329      GTTTACCACT CCCTATCAGT GATAGAGAAA AGTGAAAGTC GAGTTTACCA CTCCCTATCA      180
331      GTGATAGAGA AAAGTGAAAG TCGAGTTTAC CACTCCCTAT CAGTGATAGA GAAAAGTGAA      240
333      AGTCGAGTTT ACCACTCCCT ACCAGTGATA GAGAAAAGTG AAAGTCGAGT TTACCACTCC      300
335      CTATCAGTGA TAGAGAAAAG TGAAAGTCGA GTTTACCACT CCCTATCAGT GATAGAGAAA      360
337      AGTGAAAGTC GAGTTTACCA CTCCCTATCA GTGATAGAGA AAAGTGAAAG TCGAGCTCGG      420
339      TACCCGGGTC GAGTAGGCGT GTACGGTGGG AGGCCTATAT AAGCAGAGCT CGTTTAGTGA      480
341      ACCGTCAGAT CGCCTGGAGA CGCCATCCAC GCTGTTTGA CCTCCATAGA AGACACCGGG      540
343      ACCGATCCAG CCTCCGCGGC CCCGAATTC      569
346 (2) INFORMATION FOR SEQ ID NO: 7:
348      (i) SEQUENCE CHARACTERISTICS:
349          (A) LENGTH: 520 base pairs
350          (B) TYPE: nucleic acid
351          (C) STRANDEDNESS: double
352          (D) TOPOLOGY: linear
W--> 354      (ii) MOLECULE TYPE: DNA
357      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
359      AGATCTGCAG GGTCGCTCGG TGTTGAGGC CACACGCGTC ACCTTAATAT GCGAAGTGGA      60
361      CCGGATCTCG AGTTTACCAC TCCCTATCAG TGATAGAGAA AAGTGAAAGT CGAGTTTACC      120
363      ACTCCCTATC AGTGATAGAG AAAAGTGAAA GTCGAGTTTA CCACTCCCTA TCAGTGATAG      180
365      AGAAAAGTGA AAGTCGAGTT TACCACTCCC TATCAGTGAT AGAGAAAAGT GAAAGTCGAG      240

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/874,389

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Input Set : N:\Cr3\RULE60\09874389.txt

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:80 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:266 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:319 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:354 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:459 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:470 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12
L:481 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:492 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:503 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15
L:923 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:934 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:960 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27